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-i- SUBCELLULAR INFORMACE PROTEIN.
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                                                        PFAM; PF00546; Seedstore_7s;
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RESULT 3
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Best Local Similarity 38.0
Matches 232; Conservative
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P15590;
01-APR-1990
01-AUG-1990
15-JUL-1999
                                                                                 Zea mays (Maize).
Zea mays (Maize).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
                                                                                                                               GLB1
         by the Glb1 gene. Plant Physiol. 91
                            STRAIN=CV. INBRED LINE VA26;
Belanger F.C., Kriz A.L.;
"Molecular characterization of
                                                                                                                                          GLOBULIN-1 S
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                                                                                                                                     (Rel. 14, Created)
(Rel. 15, Last sequence update)
(Rel. 38, Last annotation update)
S ALLELE PRECURSOR (GLB1-S) (7S-LIKE).
         91:636-643(1989)
                                                                                                                                                                                                     STANDARD;
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Query Match
Best Local Similarity
Matches 210; Conser
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERPRO; IPRO011113; -- 7s; PFAM; PF00546; Seedstore_7s; Seed storage protein; Signal
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                    533
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PTW: THREE PROTEIN-PROCESSING STEPS OCCUR IN THE FORMATION OF MATURE PROTEIN FROM THE PRIMARY TRANSLATION PRODUCT.

POLYMORPHISM: THE THREE MOST COMMONLY OCCURRING GLB1 ALLELES IN THE DESIGNATION L. I. AND S FOR LARGE, INTERMEDIATE, AND SMALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: TO OTHER 75 SEED STORAGE PROTEINS (PHASEOLIN, VICILIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONVICILIN, CONGLYCININ, ETC.
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   SSGNENULLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAASRKEVEELFNSQDE
                                                                                                                                                                                                                  VLLEANDNAFVLPTHLDADAILLVIGGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYL
                                                     HRQSQGGESERERGKGRRSEEEEESSEEQEEVGQGYHTIRARLSPGTAFVVPAGHPFVAV
                                                                                  HLSGRHG----GRGGGKRHEEEEEVHYEQ------VRARLSKREAIVVLAGHPVVEV 532
                                                                                                                        QHGQLYEADARSFHDLAEHDVSVSFANITAGSMSAPLYNTRSFKIAYVPNGKGYAEIVCP
                                                                                                                                                                                                                                                                                                    INRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTERLRG
                                                                                                                                                                                                                                                                                                                                                                                                                             QRGGSGRYEEGEEKQSD-NPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRL:||:|:||:||:||:::||:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEYNRQRDPQQQYEQCQKRCQRRETEPRHMQ-ICQQRCERRYEKEKRKQQKRYEEQQRED 131
                                                                                                                                                           KYGQAYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVEMACP 485
                                                                                                                                                                                            LFGRHGQDKGIIVRATEEQTRELRRHASEGGHGPHWPLPPFGE-SRGPYSLLDQRPSIAN
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                                                                                                                                                                                                                                                                                                                                     AVLEANPRSFVVPSHTDAHCIGYVAEGEGVVTTIENGERRSYTIKQGHVFVAPAGAVTYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEKYEERMKEGDNKKDPQQREYEDCRRHCEQQEPRLQYQCQRRCQEQQRQHGRGGDLMNP 19:
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Pred.
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N-LINKED (GLCNAC. ...
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Burks A.W., Cockrell G., Stanley J.S., Helm R.M. Recombinant peanut allergen Ara h I expression patients with peanut hypersensitivity.";
J. Clin. Invest. 96:1715-1721(1995)
-: SIMILARITY: TO 7S SEED STORAGE PROTEINS (PHACONVICILIN, CONGLYCININ, ETC.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L34402; AAB00861.1; HSSP; P50477; 1CAW.
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Eukaryota; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoldeae; Arachis.
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DFFPASSRDQSSYLQGFSRNTLEAAFNAEFNEIRRVLLEENAGGEQEERGQRRWSTRSSE 359
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                                                       EFFPAGGQNPEPYLSTFSKEILEAALNTQTERLRGVL-----
                                                                                                                  QGQATVTVANGNNRKSFNLDEGHALRIPSGFISYILNRHDNQNLRVAKISMPVNTPGQFE 299
                                                                                                                                                                                                                                     RRFSTRYGNQNGRIRVLQRFDQRSRQFQNLQNHRIVQIEAKPNTLVLPKHADADNILVIQ
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Pred. No. 1.5e-46;
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SEQUENCE
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Burks A.W., Cockrell G., Stanley J.S., Helm R.M.
"Recombinant peanut allergen Ara h I expression
patients with peanut hypersensitivity.";
J. Clin. Invest. 96:1715-1721(1995)
-i- SIMILARITY: TO 75 SEED STORAGE PROTEINS (PHACONVICILIN, CONGLYCININ, ETC.).
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01-NOV-1995 (Rel. 32, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation a
ALLERGEN ARA H 1, CLONE P17 (ARA H 1).
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;

Fabales; Fabaceae; Papilionoideae; Arachis.
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01-NOV-1995
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                              CQKRCQRRETEPRHMQICQQRCERRYEKEKRKQQKRYEEQQREDEEKYEERMKEGD--NK 145
                                                                          SKYDNQEDPQTEC-QQCQRRCRQQESDPRQQQYCQRRCKEICEEEEEYNRQRDPQQQYEQ 87
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GERTRGRQPGDY----
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Sebastiani F.L., Farrel L.B., Schuler
"Complete sequence of a cDNA of alpha
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01-APR 1990 (Rel. 14, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
BETA-CONGLYCININ, ALPHA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLCA_SOYBN P13916;
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                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                  nt Mol. Biol. 15:197-201(1990).

FUNCTION: SEED STORAGE PROTEIN. ACCUMULATES DURING SEED DEVELOPMENT AND IS HYDROLYZED AFTER GERMINATION TO PROVIDE CARBON AND NITROGEN SOURCE FOR THE DEVELOPING SEEDLING. SUBUNIT: THE ALPHA'-, ALPHA-, AND BETA-SUBUNITS ASSOCIATE I VARIOUS COMBINATIONS TO FORM TRIMERIC PROTEINS.
                                                 European Bioinformatics Institute.
                                                                                                                 SIMILARITY: TO OTHER 7S SEED ST
CONVICILIN, CONGLYCININ, ETC.).
                                                                                                                                                   VACUOLAR PROTEIN BODIES.
                                                                                                                                                                    SUBCELLULAR LOCATION: EMBRYO AXIS,
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non-profit institutions as long and this statement is not removed requires a license agreement (See
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01-0CT-1989 (Rel. 1
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BETA-CONGLYCININ, &
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23, Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
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Glycine max (Soybean)
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  139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERPRO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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nes 205; Conser
                                                                                                                                                                                                                                                                                                        Match
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SUBUNIT: THE ALPHA', ALPHA', AND BETA-SUBUNITS ASSOCIATE VARIOUS COMBINATIONS TO FORM TRIMERIC PROTEINS.
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; P02853; 2PHL.
EEQDER--EHPRPHQPHQKEEE----KH-EWQHKQEKHQGKESEEEEEDQDEDEEQDKESQ
                                    EKYEERMKEGDNKRDPQQREYEDCRRHCEQQEPRLQYQCQRRCQEQQRQ-HGRGGDLMNP
                                                                               HPERERQQHGEKEEDEGEQPRPFPFPRPR--QPHQEEEHEQKEEHEWHRKEEKHGGKGSE
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                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-CV. FELTHAM FIRST;
MEDLINE-88326208; PubMed=3415641;
Bown D. Ellis T.H.N., Gatehouse J.A.;
"The sequence of a gene encoding convicilin from pea
"The sequence of a gene encoding convicilin by an
                             EMBL; X06398; CAA29695.1;
PIR; S00566; S00566.
HSSP; P02853; 2PHL.
                                                                                                                                                       or send an email to license@isb-sib.ch).
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
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01-JAN-1990 (Rel. 13, Last sequence update)
01-AUG-1990 (Rel. 15, Last annotation updat
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FT
SQ
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Matches
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                                                                                                                 SBP_SOYBN STAN
Q04672;
01-JUN-1994 (Rel. 2
01-JUN-1994 (Rel. 2
01-JUN-1994 (Rel. 2
SUCROSE-BINDING PRO
                                                            Glycine max (Soybean).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00546; Seedstore_7s; 1.
Seed storage protein; Multigene
SIGNAL 1
28
                       SEQUENCE FROM N.A., AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
         TISSUE=EMBRYO
                                                  Fabales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     YSNKYGQAYEVKPE-DYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVE 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QLRDRKRTQQGEERD-AIIKVSREQIEELRKLAKSSS----KKSLPSEFEPFNLRSHKPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKFLOTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTERLRGVL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                storage protein; Multigene family; Signal.
                                                                                                                                                                                                                                                          ASAEPEQKEEESQR---KRSPLSSVLD
                                                                                                                                                                                                                                                                                                                                                                   LL-----
                                                                                                                                                                                                                                                                                                                                                                                           MACPHLSGRHGGRGGGKRHEEEEEVHYE-----QVRARLSKREAIVVLAGHPVVFVSSG
                                                                                                                                                                                                                                                                                                                                                                                                                      YSNKFGKLFEITPEKKYPQLQDLDILVSCVEINKGALMLPHYNSRAIVVLLVNEGKGNLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SESQEHRNPFLFKSNKFLTLFENENGHIRRLQRFDKRSDLFENLQNYRLVEYRAKPHTIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SQRREDPEER-----ARLRHREER--TKRDRRH------QREGEEEERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDNKRDPQQREYEDCRRHCEQQEPRLQYQCQRRCQEQQRQHGRGGDLMNPQRGGSGRYEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E-----KEEHE------EEKQKYRYQREKKEQKEVQPGRERWEREEDEEQVEEEWRG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VTYANYD--EGSETRVPGQRERGRQ-------EGEKEEKRHGEWRPSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDWSKYDNQEDPQTECQQCQRRCRQQESDPRQQQYCQRRCKEICEEEEEYNRQRDPQQQY 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------GQQREGVIIRASQEQIRELTRDDSESRRWHIRRGGESSRGPYNLFNKRPL 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQCQKRCQRRETEPRHMQICQQRCERRYEKEKRKQQK----RYEEQQREDEEKYEERMKE 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        al Similarity
208; Conser
                                                  Fabaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          571 AA;
                                                                                                                                                                                                                                                                                                              -GFGINAKNNQRNFLSGSDDNVISQIENPVKELTFPGSSQEVNRLIKNQKQSHF:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29
                                                                                                                                                                                        STANDARD;
                                                                                                                   1. 29, Created)
1. 29, Last sequence update)
1. 29, Last annotation update
PROTEIN PRECURSOR (SBP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       571
                                                                                                                                                                                                                                                                                                                                                                  GLKNEQQEREDRKERNNEVQRYEARLSPGDVVIIPAGHPVAISASS
                                                  Papilionoideae;
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                       SEQUENCE OF
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Pred. No. 1e-4
12; Mismatches
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                                               Glycine.
                       30~50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   571;
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                                                                                                                                                                                                                                                                                                                                                                                                                       438
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MEDLINE-93104680;

PubMed=1467654;

RANGE OF THE REPORT OF THE REP

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grimes H.D., Overvoorde P.J., Ripp K., Franceschi V.R., Hitz W.D., "A 62-kD sucrose binding protein is expressed and localized in tissues actively engaged in sucrose transport.";
Plant Cell 4:1561-1574(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
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Transport; Sugar transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
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                                                                                                                                                                                          317
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SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED
TISSUE SPECIFICITY: ASSOCIATED WITH THE PLASMA MEMBRANE OF
TISSUE SPECIFICITY: ASSOCIATED WITH THE PLASMA MEMBRANE OF
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DEVELOPMENTAL STACE: IN THE COTYLEDON, EXPRESSION IS NOT DETECTED UNTIL 10 DAYS AFTER FERTILIZATION. BETWEEN 10-19 DAYS AFTER FERTILIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DAYS AFTER FERTILIZATION. 30 DAYS AFTER FERTILIZATION, NO EXPRESSION OCCURS. THIS EXPRESSION PATTERN CLOSELY PARALLELS RATE OF SUCROSE UPTAKE IN THE COTYLEDON.
ENLLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JQ1730; JQ1730.
; P50477; 1CAW.
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                                                            RGHLQISCPHMS----SRSSHSKHDKSSP-SYHRISSDLKPGMVFVVPPGHPFVTIASNK
                                                                                                                                                                                                                                                                                                          AALQTPKGKLENVFDQQNEGSIFRISREQVRALA-PTKKSSWWPF--GGE-SKPQFNIFS
                                                                                                                                                                                                                                                                                                                                                                                                                                    HIPAGTPLYIVNRDENDKLFLAMLHIPVSVSTPGKFEEFFAPGGRDPESVLSAFSWNVLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIPAGTTFYLINRDNNERLHIA--KFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILE 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLQGIENERLAILEARAHTEVSPRHEDSEVVEFNIKGRAVLGLVSESETEKITLEPGDMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLRALKNYRLVLLEANPNAFVLPTHLDADAILLVIGGRGALKMIHRDNRESYNLECGDVI 300
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                                                                                                                   EADVEMACPHLSGRHGGRGGKRHEEEEEVHYEQVRARLSKREAIVVLAGHPVVFVSSGN
                                                                                                                                                                                      KRPTISNGYGRLTEVGPDDDEKSWLQRLNLMLTFTNITQRSMSTIHYNSHATKTALVIDG
                                                                                                                                                                                                                                             KRPLYSNKYGQAYEVKPEDYRQ--LQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVVASG
                                                                                                                                                                                                                                                                                                                                                                    AALNTQTERLRGVLGQQREGVIIRASQEQIRELTRDDSESRRWHIRRGGESSRGPYNLFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HGRGGDLMNPQRGGSGRYEEGEEKQSDNPYYFDE-RSLSTRFRTEEGHISVLENFYGRSK 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KCKETEVEEE-----DPELVTCKHQCQQQQQYTEGDKR---VCLQSCD-RYHRMKQERE 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L06038; AAB03894.1; -.
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524 AA;
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60522 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 794; DB 1;
Pred. No. 2.5e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUCROSE-BINDING PROTEIN. 0251EE90796EF341 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 176; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 524;
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Ş Db Qy DЬ Qy Ф QΥ дb Ωy В Qy Вb 20 В Qy Db δÃ

Ъ δÃ

34

Matches Query Match Best Local

al Similarity 162; Conser

Conservative

80;

Mismatches 154;

35;

Gaps

Çī

93

22.8%;

Score 759.5; DB 1 Pred. No. 2.9e-40;

Length

209

NPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVLPTHLDA 268 NPFTFKSNKFQTLFENENGHTRLLQKFDQRSKTFENLQNYRLLEYKSKPHTTFLPQHTDA

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RESULT 1
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CONFLICT
SEQUENCE
                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                           CHAIN
                                                       SIGNAL
                                                              PFAM; PF00546; Seedstore_7s; 1.
Seed storage protein; Multigene family; Signal
                                                                                                                                                EMBL; X14076; CAA32239.1; EMBL; Y00722; CAA68708.1;
                                                                                                                                                                                                                  modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                              Gatehouse J.A., Wright D.J., Boulter D.; "ISOLation and expression of a pea vicilin cDNA in Saccharomyces cerevisiae."; Biochem. J. 251:857-864(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CV. FELTHAM FIRST;
MEDLINE=88326226; PubMed=3046604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Higgins T.J.V., Newbigin E.J., Spencer D., "The sequence of a pea vicilin gene and it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pisum sativum (Garden pea)
Eukaryota; Viridiplantae; I
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01-APR-1990 (Rel.
15-JUL-1999 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P13918
                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: COTYLEDONARY MEMBRANE-BOUND VACUOLAR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                   Watson M.D., Lambert N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 27-459 FROM N.A. (CLONE PDUB9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant Mol. Biol. 11:683-695(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=SEEDLING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fabales;
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                                                                                                         S00567; S00567.
S08505; S08505.
; P50477; ICAW.
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 VICILIN.

V -> L (IN REF. 2).

I -> V (IN REF. 2).

I => D (IN REF. 2).
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01-MAY-1992 (Rel. 2
01-NOV-1995 (Rel. 3
BETA-CONGLYCININ, E
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Glycine max (Soybean).
Glycine max (Soybean).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Eukaryota; viridiplantae; Embryophyta; Rosidae; eurosids I;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fahales; Fabaceae; Papilionoideae; Glycine.
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                  HSSP;
                                PIR; JQ0969; FWSYCB.
                                               EMBL; S44893; AAB23463.1;
                                                                                           use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                            the
use
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-i- FUNCTION: SEED STORAGE PROTEIN. ACCUMULATES DURING
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-93005638; pubMed-2562562;
Harada J.J., Barker S.J., Goldberg R.B.;
"Soybean beta-conglycinin genes are clustered in several DNA regions
and are regulated by transcriptional and posttranscriptional
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                                                                              send an email to license@isb-sib.ch).
                                                                                                                                                                                                   PUNCTION: SEED STORAGE PROTEIN. ACCUMULATES DURING SEED DEVELOPMENT AND IS HYDROLYZED AFTER GERNINATION TO PROVIDE CARBON AND NITROGEN SOURCE FOR THE DEVELOPING SEEDLING.
SUBUNIT: THE ALPHA', ALPHA, AND BETA-SUBUNITS ASSOCIATE I VARIOUS COMBINATIONS TO FORM TRIMERIC PROTEINS.
SUBCILLULAR LOCATION: EMBRYO AXIS, AND COTYLEDONARY MEMBRAN VACUOLAR PROTEIN BODIES.
SUBCILLULAR TO OTHER 75 SEED STORAGE PROTEINS (PHASEOLIN, VCONVICILIN, CONCLYCININ, ETC.).
                                                                                                                            European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content
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                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration -
sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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MEDLINE=88067789; PubMed=3684610;
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MEDLINE=88096511;
Weschke W., Baeum
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Eukaryota; Viridiplantae;
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EMBL; Y00462; CAA68525.1; -
PIR; S06309; S06309.
PIR; A27288; A27288.
HSSP; P50477; ICAW.
     P02854;
21-JUL-1986
21-JUL-1986
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-!- SUBC
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SIMILARITY:
CONVICILIN,
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FUNCTION: SEED STORAGE PROTEIN.
SUBCELLULAR LOCATION: COTYLEDONARY MEMBRANE-BOUND VACUOLAR PROTEIN
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SEQUENCE
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Pisum sativum (Garden pea).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The vicilin gene family of pea (Pisum sativum L.): a coding sequence for preprovicilin.", Nucleic Acids Res. 11:2367-2380(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CV. FELTHAM FIRST;
MEDLINE=83220791; PubMed=6687941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fabales; Fabaceae; Papilionoideae; Pisum.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1990 (Rel. 13, Last annotation update) PROVICILIN PRECURSOR (TYPE B) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boulter D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERPRO; IPRO01113; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: COTYLEDONARY MEMBRANE-BOUND VACUOLAR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lycett G.W., Delauney A.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BODIES
                                                                                                                                                                                                                                                                                                                                                                                                                             ; PF00546; Seedstore_7s; 1. storage protein; Glycoprotein; Multigene family;
                                                                                                                                                        NAQNNHENFLAGRERNVLQQIEPQAMELAFAASRKEVE
                                                                NENQGKENDKEEEQEEETSKQVQLYRAKLSPGDVFVIPAGHPVAINASSDLNLI--GLGI
                                                                                                    GRHGGRGGGKRHEEEEEEV--HYEQVRARLSKREAIVVLAGHPVVFVSSGNENLLLFAFGI
                                                                                                                                  KFFEITPEKNQQLQDLDIFVNSVDIKVGSLLLPNYNSRAIVIVTVTEGKGDFELVGQR--
                                                                                                                                                                                                      DRRQEINEENVIVKVSRDQIEELSKNAKSSS----KKSVSSESGPFNLRSRNPIYSNKFG
                                                                                                                                                                                                                        -----EGVIIRASQEQIRELTRDDSESRRWHIRRGGESSRGPYNLFNKRPLYSNKYG
                                                                                                                                                                                                                                                                       VNKPGQLQSFLLSGTQNQKSSLSGFSKNILEAAFNTNYEEIEKVLLEQQEQEPQHRRSLK
                                                                                                                                                                                                                                                                                                                                         ADFILVVLSGKATLTVLKSNDRNSFNLERGDAIKLPAGSIAYFANRDDNEEPRVLDLAIP
                                                                                                                                                                                                                                                                                                                                                           ADAILLVIGGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYLINRDNNERLHIAKFLQT
                                                                                                                                                                                                                                                                                                                                                                                                             ENPFIFKSNRFQTLYENENGHIRLLQKFDKRSKIFENLQNYRLLEYKSKPHTLFLPQYTD
NAENNERNFLAGEEDNVISQVERPVKELAFPGSSHEVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151;
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51; Conservative
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221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 712.5; 1
Pred. No. 2e-3'
76; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEED STORAGE
, ETC.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gatehouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLEAVAGE (POTENTIAL).
N-LINKED (GLCNAC. . .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 712.5; DB 1;
No. 2e-37;
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                                584
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409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gilroy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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34, Created)
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STANDARD;

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Query Match
Best Local Similarity
Matches 144; Conser
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SEQUENCE
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Canavalia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents to the content is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Canavalia ensiformis (Jack bean) (Horse Eukaryota; Viridiplantae; Embryophyta; 1 Magnoliophyta; eudicotyledons; core eudi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ko T.-P., Ng J.D., McPherson A.; "The three-dimensional structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94143476; PubMed=8310056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ensiformis)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=COTYLEDON;
MEDLINE=94143475; PubMed=8310055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ng J.D., Stinchcombe T., Ko T.-P., Alexander E., McPhersor "PCR cloning of the full-length cDNA for the seed protein from the jack bean plant, Canavalis ensiformis."; Plant Mol. Biol. 18:147-149(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERPRO; IPRO01113; -. PFAM; PF00546; Seedstore_7s; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant Physiol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ensiformis) canavalin.";
Plant Physiol. 101:713-728(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92119225; PubMed=1731967; Ng J.D., Stinchcombe T., Ko T.-P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=COTYLEDON;
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    212
                                                                                    152
                                                                                                                           314
                                                                                                                                                                                                           254
                                                                                                                                                                                                                                                                                        194 GGSGRYEEGEEKQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       %L; X59467; CAA42075.1; ...
$; ICAU; 31-0CT-93.
$; ICAV; 31-0CT-93.
$; ICAN; 31-0CT-93.
$; ICAN; 31-0CT-93.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: HOMOTRIMER.
SIMILARITY: TO OTHER 7S SEED ST
CONVICILIN, CONGLYCININ, ETC.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: SEED STORAGE PROTEIN
                                                                                                     DNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTERL-RGVL 372
QEEQEGVIVKMPKDQIQEISKHAQSSSRKTL---
                                      GQQREGVIIRASQEQIRELTRDDSESRRWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYE
                                                                                DNNQNLRILKFAITFRRPGTVEDFFLSSTKRLPSYLSAFSKNFLEASYDSPYDEIEQTLL
                                                                                                                                                                 CSKPNTLLLPHHSDSDLLVLVLEGQAILVLVNPDGRDTYKLDQGDAIKIQAGTPFYLINP
                                                                                                                                                                                                       EANPNAFVLPTHLDADAILLVIGGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYLINR 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                storage protein; Signal;
                                                                                                                                                                                                                                                  GGEAEDESEESRAQNNPYLFRSNKFLTLFKNQHGSLRLLQRFNEDTEKLENLRDYRVLEY 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fabaceae; Papilionoideae; Canavalia.
                                                                                                                                                                                                                                                                                                                                                                                                                            27
445
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445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; 3D-structure.
BY SIMILARITY.
CANAVALIN.
                                                                                                                                                                                                                                                                                                                                Score 692.5; DB 1
Pred. No. 3.9e-36;
9; Mismatches 160
                                                                                                                                                                                                                                                                                                                                                                                                                                      30383C5F83A1E9B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STORAGE PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ta; Tracheophyta; Spermatophyta;
eudicots; Rosidae; eurosids I;
  SSQDKPFNLRSRDPIYSNNYGKLYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bean)
                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                  160;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PHASEOLIN,
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                                                                                                                                                                                                                                                                                                                                Gaps
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     CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "CDNAS for canavalin and concanavalin A from Canavalia gladiata seeds. Nucleotide sequence of cDNA for canavalin and RNA blot analysis of canavalin and concanavalin A mRNAs in developing see Eur. J. Biochem. 170:515-520(1988).
                                                                                                         Seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Canavalia gladiata (Sword bean) (Japanese jack bean).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; S
Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CANAVALIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1989 (Rel. 01-JUL-1989 (Rel. 01-OCT-1996 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P10562;
01-JUL-1989
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                                                       CHAIN
                                                                                  SIGNAL
                                                                                                       PFAM; PF00546; Seedstore_7s;
Seed storage protein; Signal.
                                                                                                                                                                                                                             EMBL; X06733; CAA29910.1; -. EMBL; X15076; CAA33172.1; -.
                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Takei Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=89296493; PubMed=2740227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=SEED;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=88111636; PubMed=3338449; Yamauchi D., Nakamura K., Asahi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fabales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     raker r., ramauchi D.,
"Nucleotide sequence o
                                                                                                                                                      (NTERPRO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leic Acids Res. 17:4381-4381(1989).
FUNCTION: SEED STORAGE PROTEIN.
SUBJUNIT: HOMOTRIMER.
SIMILARITY: TO OTHER 7S SEED STORAGE
CONVICILIN, CONGLYCININ, ETC.).
                                                                                                                                                                                                      S00281;
                                                                                                  storage protein;
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433 RRAHLP 438
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                   610 TKQQQP 615
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